

EXHIBIT A

Sequence alignment (SEQ ID NO:1 top and SEQ ID NO:3 bottom)

>
>
scoring matrix: , gap penalties: -12/-2
92.0% identity; Global alignment score: 3006

861 nt vs.
796 nt

10	20	30	40	50	60
935757	ATGAAACAGTTGAAATCATCGCAGAAGGATAAAAGTTCGTCAGTTATGATCTTCACACAA				
-	-----	CGTCAGTTATGATCTTCACACAA			
10	20				
70	80	90	100	110	120
935757	TCTAGTAAAAAACAGCAGTAAGTTGCTTTCTCAAATGACTGGAAGTTAGATGTTGCA				
-	-----	TCTAGTAAAAAACAGCAGTAAGTTGCTTTCTCAAATGACTGGAAGTTAGATGTTGCA			
30	40	50	60	70	80
130	140	150	160	170	180
935757	ACAGATAATTTTTCCAAAATCCTGAACCTTATATACAGAGAGAGTGTAAAGGATCATTG				
-	-----	ACAGATAATTTTTCCAAAATCCTGAACCTTATATACAGAGAGAGTGTAAAGGATCATTG			
90	100	110	120	130	140
190	200	210	220	230	240
935757	GACAGGAAGAAGTTAGAACAGCTGTACAAATAGATACAAAGACCCCTCAAGATGAGAATAAA				
-	-----	GACAGGAAGAAGTTAGAACAGCTGTACAAATAGATACAAAGACCCCTCAAGATGAGAATAAA			
150	160	170	180	190	200
250	260	270	280	290	300
935757	ATTGGAATAGATGGCATACAGCAGTTCTGTGATGACCTGGCACTCGATCCAGCCAGCATT				
-	-----	ATTGGAATAGATGGCATACAGCAGTTCTGTGATGACCTGGCACTCGATCCAGCCAGCATT			
210	220	230	240	250	260
310	320	330	340	350	360
935757	AGTGTGTTGATTATTGCATGGAAGTTAGAGCAGCAACACAGTGGAGTTCTCCAAACAG				
-	-----	AGTGTGTTGATTATTGCATGGAAGTTAGAGCAGCAACACAGTGGAGTTCTCCAAACAG			
270	280	290	300	310	320
370	380	390	400	410	420
935757	GAGTTCATGGATGGCATGACAGAATTAGGATGTCAGCATGAGAAAACATAAGGCCAG				
-	-----	GAGTTCATGGATGGCATGACAGAATTAGGATGTCAGCATGAGAAAACATAAGGCCAG			
330	340	350	360	370	380
430	440	450	460	470	480
935757	ATACCCAAGATGGAACAAGAATTGAAAGAACCGAGGACGATTTAAGGATTTACCAAGTT				

	ATACCCAAGATGGAACACAAGAATTGAAAGAACCGAGCAGTTAAGGATTTCAGCTT
390	400
410	420
430	440
490	500
510	520
530	540
935757 ACTTTTAATTTGCAAGAACATCCAGGACAAAAAGGATTAGATCTAGAAATGGCCATTGCC	
450	460
470	480
490	500
550	560
570	580
590	600
935757 TACTGGAACCTTAGTGCTTAATGGAAGATTAAATTCTAGACTTATGGAATAATTTCG	
510	520
530	540
550	560
610	620
630	640
650	660
935757 TTGGAACATCATAAACGATCAATACCAAAAGACACTTGGAACTCTCTTTAGACTTCAGT	
570	580
590	600
610	620
670	680
690	700
710	720
935757 ACGATGATTGCGAGATGACATGCTAATTATGATGAAAGAAGGAGCATGCCCTGTTCTTATT	
630	640
650	660
670	680
730	740
750	760
770	780
935757 GATGACTTTGGAATTGACGCCCTCAAATTGCTGGGACAAAAAGTACACAGTGTAG	
690	700
710	720
730	740
790	800
810	820
830	840
935757 CACTAAAGGAACCTCTAGAATGTACATAGTCTGTACAATAATACAAACAGAAATTGCA	
750	760
770	780
790	
850	860
935757 CAGTCATTTCTGCTGGCTGG	

Elapsed time: 0:00